

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/568,488
Source: IFWP
Date Processed by STIC: 2/23/06

ENTERED

RAW SEQUENCE LISTING

DATE: 02/23/2006

PATENT APPLICATION: US/10/568,488

TIME: 07:58:36

Input Set : A:\ISPH0859USASEQ.txt

Output Set: N:\CRF4\02232006\J568488.raw

4 <110> APPLICANT: Monia, Brett P.
5 Dobie, Kenneth W.
6 Freier, Susan M.
7 Popoff, Ian
8 Wong, Wai Shiu Fred
9 Karras, James G.
11 <120> TITLE OF INVENTION: Antisense Modulation of p38 Mitogen
12 Activated Protein Kinase Expression
14 <130> FILE REFERENCE: ISPH-0859USA
C--> 17 <140> CURRENT APPLICATION NUMBER: US/10/568,488
C--> 17 <141> CURRENT FILING DATE: 2006-02-14
17 <150> PRIOR APPLICATION NUMBER: PCT/US2004/026344
18 <151> PRIOR FILING DATE: 2004-08-12
20 <150> PRIOR APPLICATION NUMBER: US 10/641,455
21 <151> PRIOR FILING DATE: 2003-08-15
25 <160> NUMBER OF SEQ ID NOS: 412
27 <170> SOFTWARE: FastSEQ for Windows Version 4.0
29 <210> SEQ ID NO: 1
30 <211> LENGTH: 1539
31 <212> TYPE: DNA
32 <213> ORGANISM: Homo sapiens
34 <220> FEATURE:
35 <221> NAME/KEY: CDS
36 <222> LOCATION: (295)..(1377)
38 <300> PUBLICATION INFORMATION:
39 <303> JOURNAL: Science
40 <304> VOLUME: 265
41 <305> ISSUE: 5173
42 <306> PAGES: 808-811
43 <307> DATE: 1994-08-05
44 <308> DATABASE ACCESSION NO: L35253
45 <309> DATABASE ENTRY DATE: 1995-08-14
47 <400> SEQUENCE: 1
48 ggaattccgg gcccggtctt tcctcccgcc gccgccggcc tgggtcccggt gactggcctc 60
49 cacgtccgac tcgtccgagc tgaagcccag cagcactttg ctgccagccg cggggggcggc 120
50 ggaggcgccc ccggggccctc ccaggagggt ctctggggcca gaggccgaga ttcggcacag 180
51 gccccccagga gtccgtaagt aggagagggt gcccgagacc ggccggaccc ccatccccgc 240
52 ggccgcccgc gccgctgggt ccgcggctgc gaccgtggcg gctgccgctg gaaa atg 297
53 Met
54 1
56 tct cag gag agg ccc acg ttc tac cgg cag gag ctg aac aag aca atc 345
57 Ser Gln Glu Arg Pro Thr Phe Tyr Arg Gln Glu Leu Asn Lys Thr Ile
58 5 10 15

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60	tgg	gag	gtg	ccc	gag	cgt	tac	cag	aac	ctg	tct	cca	gtg	ggc	tct	ggc	393
61	Trp	Glu	Val	Pro	Glu	Arg	Tyr	Gln	Asn	Leu	Ser	Pro	Val	Gly	Ser	Gly	
62			20					25					30				
64	gcc	tat	ggc	tct	gtg	tgt	gct	gct	ttt	gac	aca	aaa	acg	ggg	tta	cgt	441
65	Ala	Tyr	Gly	Ser	Val	Cys	Ala	Ala	Phe	Asp	Thr	Lys	Thr	Gly	Leu	Arg	
66		35					40				45						
68	gtg	gca	gtg	aag	aag	ctc	tcc	aga	cca	ttt	cag	tcc	atc	att	cat	gcg	489
69	Val	Ala	Val	Lys	Lys	Leu	Ser	Arg	Pro	Phe	Gln	Ser	Ile	Ile	His	Ala	
70	50					55				60					65		
72	aaa	aga	acc	tac	aga	gaa	ctg	cgg	tta	ctt	aaa	cat	atg	aaa	cat	gaa	537
73	Lys	Arg	Thr	Tyr	Arg	Glu	Leu	Arg	Leu	Leu	Lys	His	Met	Lys	His	Glu	
74				70					75				80				
76	aat	gtg	att	ggg	ctg	ttg	gac	gtt	ttt	aca	cct	gca	agg	tct	ctg	gag	585
77	Asn	Val	Ile	Gly	Leu	Leu	Asp	Val	Phe	Thr	Pro	Ala	Arg	Ser	Leu	Glu	
78			85				90				95						
80	gaa	ttc	aat	gat	gtg	tat	ctg	gtg	acc	cat	ctc	atg	ggg	gca	gat	ctg	633
81	Glu	Phe	Asn	Asp	Val	Tyr	Leu	Val	Thr	His	Leu	Met	Gly	Ala	Asp	Leu	
82		100					105				110						
84	aac	aac	att	gtg	aaa	tgt	cag	aag	ctt	aca	gat	gac	cat	gtt	cag	ttc	681
85	Asn	Asn	Ile	Val	Lys	Cys	Gln	Lys	Leu	Thr	Asp	Asp	His	Val	Gln	Phe	
86		115					120				125						
88	ctt	atc	tac	caa	att	ctc	cga	ggg	cta	aag	tat	ata	cat	tca	gct	gac	729
89	Leu	Ile	Tyr	Gln	Ile	Leu	Arg	Gly	Leu	Lys	Tyr	Ile	His	Ser	Ala	Asp	
90	130					135				140				145			
92	ata	att	cac	agg	gac	cta	aaa	cct	agt	aat	cta	gct	gtg	aat	gaa	gac	777
93	Ile	Ile	His	Arg	Asp	Leu	Lys	Pro	Ser	Asn	Leu	Ala	Val	Asn	Glu	Asp	
94				150					155				160				
96	tgt	gag	ctg	aag	att	ctg	gat	ttt	gga	ctg	gct	cgg	cac	aca	gat	gat	825
97	Cys	Glu	Leu	Lys	Ile	Leu	Asp	Phe	Gly	Leu	Ala	Arg	His	Thr	Asp	Asp	
98			165				170				175						
100	gaa	atg	aca	ggc	tac	gtg	gcc	act	agg	tgg	tac	agg	gct	cct	gag	atc	873
101	Glu	Met	Thr	Gly	Tyr	Val	Ala	Thr	Arg	Trp	Tyr	Arg	Ala	Pro	Glu	Ile	
102			180				185				190						
104	atg	ctg	aac	tgg	atg	cat	tac	aac	cag	aca	gtt	gat	att	tgg	tca	gtg	921
105	Met	Leu	Asn	Trp	Met	His	Tyr	Asn	Gln	Thr	Val	Asp	Ile	Trp	Ser	Val	
106		195					200				205						
108	gga	tgc	ata	atg	gcc	gag	ctg	ttg	act	gga	aga	aca	ttg	ttt	cct	ggg	969
109	Gly	Cys	Ile	Met	Ala	Glu	Leu	Leu	Thr	Gly	Arg	Thr	Leu	Phe	Pro	Gly	
110	210					215				220				225			
112	aca	gac	cat	att	gat	cag	ttg	aag	ctc	att	tta	aga	ctc	gtt	gga	acc	1017
113	Thr	Asp	His	Ile	Asp	Gln	Leu	Lys	Leu	Ile	Leu	Arg	Leu	Val	Gly	Thr	
114				230					235				240				
116	cca	ggg	gct	gag	ctt	ttg	aag	aaa	atc	tcc	tca	gag	tct	gca	aga	aac	1065
117	Pro	Gly	Ala	Glu	Leu	Leu	Lys	Lys	Ile	Ser	Ser	Glu	Ser	Ala	Arg	Asn	
118			245						250				255				
120	tat	att	cag	tct	ttg	act	cag	atg	cgg	aag	atg	aac	ttt	gcg	aat	gta	1113
121	Tyr	Ile	Gln	Ser	Leu	Thr	Gln	Met	Pro	Lys	Met	Asn	Phe	Ala	Asn	Val	
122			260				265				270						
124	ttt	att	ggg	gcc	aat	ccc	ctg	gct	gtc	gac	ttg	ctg	gag	aag	atg	ctt	1161

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```

125 Phe Ile Gly Ala Asn Pro Leu Ala Val Asp Leu Leu Glu Lys Met Leu
126      275      280      285
128 gta ttg gac tca gat aag aga att aca gcg gcc caa gcc ctt gca cat      1209
129 Val Leu Asp Ser Asp Lys Arg Ile Thr Ala Ala Gln Ala Leu Ala His
130 290      295      300      305
132 gcc tac ttt gct cag tac cac gat cct gat gat gaa cca gtg gcc gat      1257
133 Ala Tyr Phe Ala Gln Tyr His Asp Pro Asp Asp Glu Pro Val Ala Asp
134      310      315      320
136 cct tat gat cag tcc ttt gaa agc agg gac ctc ctt ata gat gag tgg      1305
137 Pro Tyr Asp Gln Ser Phe Glu Ser Arg Asp Leu Leu Ile Asp Glu Trp
138      325      330      335
140 aaa agc ctg acc tat gat gaa gtc atc agc ttt gtg cca cca ccc ctt      1353
141 Lys Ser Leu Thr Tyr Asp Glu Val Ile Ser Phe Val Pro Pro Leu
142      340      345      350
144 gac caa gaa gag atg gag tcc tga gcacctgggt tctgttctgt tgatccact      1407
145 Asp Gln Glu Glu Met Glu Ser
146      355      360
148 tcaactgtgag gggaaggcct ttccacggga actctccaaa tattattcaa gtgcctcttg      1467
149 ttgcagagat ttctccatg gtggaagggg gtgtgcgtgc gtgtgcgtgc gtgttagtgt      1527
150 gtgtgcatgt gt      1539
153 <210> SEQ ID NO: 2
155 <400> SEQUENCE: 2
W--> 156 000
159 <210> SEQ ID NO: 3
160 <211> LENGTH: 20
161 <212> TYPE: DNA
162 <213> ORGANISM: Artificial Sequence
164 <220> FEATURE:
165 <223> OTHER INFORMATION: antisense sequence
167 <400> SEQUENCE: 3
168 aagaccgggc ccggaattcc      20
170 <210> SEQ ID NO: 4
171 <211> LENGTH: 30
172 <212> TYPE: DNA
173 <213> ORGANISM: Artificial Sequence
175 <220> FEATURE:
176 <223> OTHER INFORMATION: antisense sequence
178 <400> SEQUENCE: 4
179 gtggaggcca gtccccggga ccggaattcc      30
182 <210> SEQ ID NO: 5
183 <211> LENGTH: 20
184 <212> TYPE: DNA
185 <213> ORGANISM: Artificial Sequence
187 <220> FEATURE:
188 <223> OTHER INFORMATION: antisense sequence
190 <400> SEQUENCE: 5
191 tggcagcaaa gtgctgctgg      20
194 <210> SEQ ID NO: 6
195 <211> LENGTH: 20

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```

196 <212> TYPE: DNA
197 <213> ORGANISM: Artificial Sequence
199 <220> FEATURE:
200 <223> OTHER INFORMATION: antisense sequence
202 <400> SEQUENCE: 6
203 cagagagcct cctgggaggg                20
206 <210> SEQ ID NO: 7
207 <211> LENGTH: 20
208 <212> TYPE: DNA
209 <213> ORGANISM: Artificial Sequence
211 <220> FEATURE:
212 <223> OTHER INFORMATION: antisense sequence
214 <400> SEQUENCE: 7
215 tgtgccgaat ctggcctct                20
218 <210> SEQ ID NO: 8
219 <211> LENGTH: 20
220 <212> TYPE: DNA
221 <213> ORGANISM: Artificial Sequence
223 <220> FEATURE:
224 <223> OTHER INFORMATION: antisense sequence
226 <400> SEQUENCE: 8
227 ggtctcgggc gacctctct                20
229 <210> SEQ ID NO: 9
230 <211> LENGTH: 20
231 <212> TYPE: DNA
232 <213> ORGANISM: Artificial Sequence
234 <220> FEATURE:
235 <223> OTHER INFORMATION: antisense sequence
237 <400> SEQUENCE: 9
238 cagccgcggg accagcggcg                20
241 <210> SEQ ID NO: 10
242 <211> LENGTH: 20
243 <212> TYPE: DNA
244 <213> ORGANISM: Artificial Sequence
246 <220> FEATURE:
247 <223> OTHER INFORMATION: antisense sequence
249 <400> SEQUENCE: 10
250 cattttccag cggcagccgc                20
253 <210> SEQ ID NO: 11
254 <211> LENGTH: 20
255 <212> TYPE: DNA
256 <213> ORGANISM: Artificial Sequence
258 <220> FEATURE:
259 <223> OTHER INFORMATION: antisense sequence
261 <400> SEQUENCE: 11
262 tcctgagaca tttccagcg                20
265 <210> SEQ ID NO: 12
266 <211> LENGTH: 20
267 <212> TYPE: DNA

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```

268 <213> ORGANISM: Artificial Sequence
270 <220> FEATURE:
271 <223> OTHER INFORMATION: antisense sequence
273 <400> SEQUENCE: 12
274 ctgccggtag aacgtgggccc                20
277 <210> SEQ ID NO: 13
278 <211> LENGTH: 20
279 <212> TYPE: DNA
280 <213> ORGANISM: Artificial Sequence
282 <220> FEATURE:
283 <223> OTHER INFORMATION: antisense sequence
285 <400> SEQUENCE: 13
286 gtaagcttct gacatttcac                20
288 <210> SEQ ID NO: 14
289 <211> LENGTH: 20
290 <212> TYPE: DNA
291 <213> ORGANISM: Artificial Sequence
293 <220> FEATURE:
294 <223> OTHER INFORMATION: antisense sequence
296 <400> SEQUENCE: 14
297 tttaggtccc tgtgaattat                20
300 <210> SEQ ID NO: 15
301 <211> LENGTH: 20
302 <212> TYPE: DNA
303 <213> ORGANISM: Artificial Sequence
305 <220> FEATURE:
306 <223> OTHER INFORMATION: antisense sequence
308 <400> SEQUENCE: 15
309 atgttcttcc agtcaacagc                20
312 <210> SEQ ID NO: 16
313 <211> LENGTH: 20
314 <212> TYPE: DNA
315 <213> ORGANISM: Artificial Sequence
317 <220> FEATURE:
318 <223> OTHER INFORMATION: antisense sequence
320 <400> SEQUENCE: 16
321 taaggaggtc cctgctttca                20
324 <210> SEQ ID NO: 17
325 <211> LENGTH: 20
326 <212> TYPE: DNA
327 <213> ORGANISM: Artificial Sequence
329 <220> FEATURE:
330 <223> OTHER INFORMATION: antisense sequence
332 <400> SEQUENCE: 17
333 aaccaggtgc tcaggactcc                20
336 <210> SEQ ID NO: 18
337 <211> LENGTH: 20
338 <212> TYPE: DNA
339 <213> ORGANISM: Artificial Sequence

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:172; N Pos. 429

VERIFICATION SUMMARY

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L:17 M:270 C: Current Application Number differs, Replaced Current Application No
L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:156 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (2) SEQUENCE:
L:989 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (46) SEQUENCE:
L:1184 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (62) SEQUENCE:
L:3006 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:172 after pos.:420